1 of 55

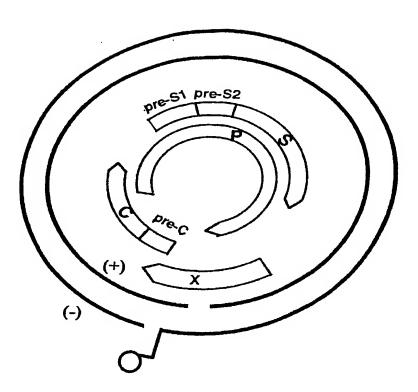


Figure 1

Figure 2

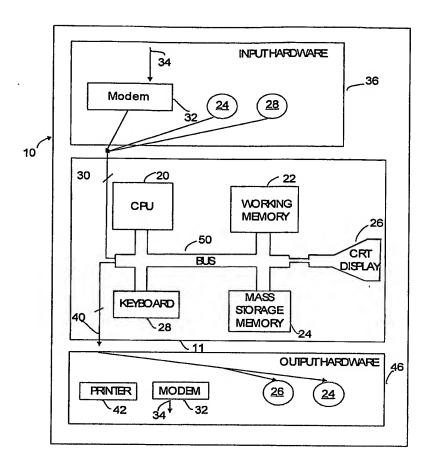


Figure 3A

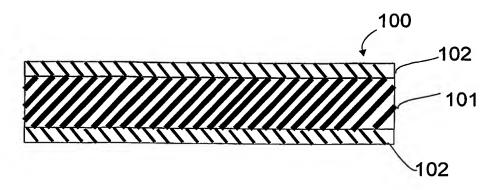


Figure 3B

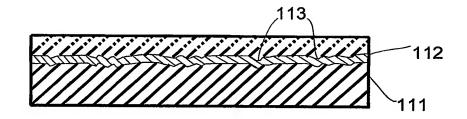


Figure 3C

Figure	4:	Patient A nt	sequence			
		10	20	30	40	50
		GCTTCCACCA	ATCGGCAGGC	AGGAAGACAG	CCTACTCCCA:	CTCTCCACC
		60	70	80	90	100
				AGGCCATGCA(₽₽ ₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽	100
					JIGGMACICC!	CACATTCC
		110		130	140	150
		ACCATGCTCT	GCTAGATCCC	AGACCTGCTG	STGGCTCCAGT	TCCGGAACA
		160			190	200
		GTAAACCCTG	TTCCGACTAC'	FGCCTCTCCC#	ATATCGTCAAT	CTTCTCGAG
		. 210	220	020		_
			220 רכייהרהרה מ	230 ATATGGAGAGC	240	250
		0.101000010	CCIGCGCCGA	JUNUNUNUN	ACCACATCAG	GATTCCTAG
		260	270	280	290	300
		GACCCCTGCT	CGTGTTACAG	GCGGGGTTTT	CTTGTTGACA	OOC OTOOTAADA
		310		330	340	350
		ACAATACCAA	AGAGTCTAGAC	CTCGTGGTGGA	CTTCTCTCAA	TTTTCTAGG
		240				
		360			390	400
		GGGAGCACCC.	ACGTGTCCTGG	SCCAAAATTTG	CAGTCCCCAA	CCTCCAATC
	•	410	120	430	440	450
		ACTCACCAAC	₽₽₽ ₽₽₽₽₽₽₽₽₽₽₽₽₽	₽₽₽ ₽₽₽₽₽₽₽₽₽₽₽	44U ™CC™™™™CCC	450
				,011111110100	IGGITATCGC	IGGAIGIGI
		460	470	480	490	500
		CTGCGGCGTT'	TATCATCTTC	CTCTTCATCC	TGCTGCTATG	CCTCATCTT
		510	520	530	540	550
		CTTGTTGGTT	CTTCTGGACTA	CCAAGGTATG	TTGCCCGTTT	GTCCTCTAC
		5.60	570	500		
		TTCCAGGAAC	O/U מייים מייים מייים מייים	580	590	600
		1100MOMAC	TOMOTACOA	GCACGGGACC,	ATGCAAGACC	TGCACGACT
		610	620	630	640	650
		CCTGCTCAAG			GTTGCTGTAC	りこり つででつつな ム なA
		660	670	680	690	700
		GGACGGAAATI	GCACTTGTAT	TCCCATCCCA:	rcatcttggg(CTTTCGTAA
		= -				
	-	710	720	730	740	75_0
		GATTCCTATGO	GAGTGGGCCT	CAGTCCGTTT	CTCCTGGTTC	AGTTTACTA
		760	770	700	700	222
		GTGCCATTTGT		780 GTAGGGCTTT	790 CCCCACTGT	800
			- 0110100110	O+MGGGCITI(CCCCACIGT	LIGGUTTTC
		810	820	830	840	850

6 of 55

AGTTATATGGATGATGTGGTATTGGGGGCCCAAGTCTGTACAACATCTTGA 870 880 890 900 ATCCCTTTATACCGCTATTACCAATTTTCTTTTGTCTTTGGGTATACATT 920 930 TAAACCCTAATAAAACCAAGCGTTGGGGCTACTCCCTTAACTTCATGGGA 960 970 980 990 1000 TATGTAATTGGAAGTTGGGGTACCTTGCCACAGGAACATATTGTACAAAA AATCAAA

7 of 55

Figure 5: Patient A. HBV Polymerase sequence

10	20	30	40	50
EDWGPCAEYGEHHIRI	PRTPARV	TGGVFLVDKNP	HNTKESRLVV	DFSQFS
60	70	80	90	100
RGSTHVSWPKFAVPNI	QSLTNLL	SSNLSWLSLDV	SAAFYHLPLH	IPAAMPH
110	120	130	140	150
LLVGSSGLPRYVARLS	STSRNIN	YQHGTMQDLHD	SCSRNLYVSI	LLLYKT
160		· 180	190	200
FGRKLHLYSHPIILGF	RKIPMGV	GLSPFLLVQFT	SAICSVVRRA	FPHCLA
210	220	230	240	250
FSYMDDVVLGAKSVQH	LESLYTA	ITNFLLSLGIH	LNPNKTKRWG	YSLNFM
260	270			
GYVIGSWGTLPQEHIV	QKIK			

Figure 5

8 of 55

Figure 6: Patient A HBV HbsAg sequence

MESTTSGFLGPLLVLQAGFFLLTRILTIPKSLDSWWTSLNFLGGAPTCPG QNLQSPTSNHSPTSCPPICPGYRWMCLRRFIIFLFILLLCLIFLLVLLDY QGMLPVCPLLPGTSTTSTGPCKTCTTPAQGTSMFPSCCCTKPSDGNCTCI PIPSSWAFVRFLWEWASVRFSWFSLLVPFVQWFVGLSPTVWLSVIWMMWY WGPSLYNILNPFIPLLPIFFCLWVYI

9 of 55

Figure 7: Patient B HBV NT sequence

10		30	40	50
TCTGTCTCCACCTI		CTCATCCTCAC	GCCATGCAGI	TGGAACT
60	70	80	90	100
CCACAACCTTCCAC	CCAAACTCTG	CAAGATCCCAC	SAGTGAGAGGC	CCTGTAT
110	120	130	140	150
TTCCCTGCTGGTGG	GCTCCAGTTC	AGGAACAGTAA	AACCCTGTTCC	CGACTTC
160	170	180	190	200
TGTCTCTCACACAT	CGTCAATCT	CTCGAGGAT	GGGGTCCCT	ECGCTGA
210	220	230	240	250
ACATGGAGAACATO	CACATCAGGAT	TTCCTAGGACO	CCCTGCTCGT	STTACAG
260	270	280	290	300
GCGGGGTTTTTCTT	'GTTGACAAG	AATCCTCACAA	ATACCGCAGAG	STCTAGA
310	320	330	340	350
CTCGTGGTGGACTT	CTCTCAATT	TTCTAGGGGG	ACTACCGTGT	GTCTTG
360	370	380	390	400
GCCAAAATTCGCAG	TCCCCAACCT	CCAATCACTO	CACCAACCTCC	TGTCCT
410	420	430	440	450
CCAACTTGTCCTGG	TTATCGCTG	SATGTATCTGO	CGGCGTTTTAT	CATCTT
460	470	480	490	500
CCTCTTCATCCTGC	TGCTATGCCT	CATCTTCTT	STTGGTTCTTC	TGGACT
510	520	530	540	550
ATCAAGGTATGTTG	CCCGTTTGTC	CCTCTAATTCC	CAGGATCTTCA	ACCACC
560	570	580	590	600
AGCACGGGACCATG	CAGAACCTGO	CACGACTCCTG	GCTCAAGGAAA	CTCTAT
610	620	630	640	650
GTATCCCTCCTGTT	GCTGTACCA	ACCTTCGGAC	CGGAAATTGCA	CCTGTA
660	670	680	690	700
TTCCCATCCCATCA	TCCTGGGCTT	TCGGAAAATT	CCTATGGGAG	TGGGCC
710 TCAGCCCGTTTCTC		- 730 TTACTAGTGC		750 GTGGTT

Figure 7

10 of 55

760 770 780 790 80	00
CGTAGGGCTTTCCCCCACTGTTTGGCTTTCAGTTATATGGATGATGTGG	2Ф
	3
810 820 830 840 85	50
ATTGGGGGCCAAGTCTGTATCGCATCTTGAGTCCCTTTTTACCGCTGTT	ľ.A
860 870 880 890 90	20
3,0	
CCAATTTCTTTTGTCTTTGGGTATACATTTAAACCCTCACAAAACAAA	AΑ
910 920 930 940 95	50
AGATGGGGTCACTCTTTACATTTCATGGGCTATGTCATTGGATGTTATG	70
MONTGOOGLEACTCTTTACATTTCATGGGCTATGTCATTGGATGTTATG	36
960 970 980	
GTCATTGCCACAAGATCACATCAGACAGAAAA	

Figure 7 continued

11 of 55

Figure	8:	Patient	В	POLYMERASE	sequence
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EDWGPCA	10	20	30	40	50
	EHGEHHIRI	PRTPARVTGGV	FLVDKNPHNI	TAESRLVVDFS	SQFS
RGNYRVS	60	70	80	90	100
	WPKFAVPNLO	QSLTNLLSSNI	SWLSLDVSA	AFYHLPLHPAA	MPH
	110	120	130	140	150
	LSRYVARLS:	SNSRIFNHQHG	TMQNLHDSCS	SRKLYVSLLLI	YQT
	160	170	180	190	200
	YSHPIILGFI	RKIPMGVGLSP	FLLAQFTSAI	CSVVRRAFPH	CLA
	210 VLGAKSVSHI	220 SESLFTAVTNF	230 LLSLGIHLNE	240 PHKTKRWGHSL	250 HFM
	260 GSLPQDHIR(ΣK			

12 of 55

Figure 9:Patient B HBsAG sequence

MENITSGFLGPLLVLQAGFFLLTRILTIPQSLDSWWTSLNFLGGTTVCLG QNSQSPTSNHSPTSCPPTCPGYRWMYLRRFIIFLFILLLCLIFLLVLLDY QGMLPVCPLIPGSSTTSTGPCRTCTTPAQGNSMYPSCCCTKPSDGNCTCI PIPSSWAFGKFLWEWASARFSWLSLLVPFVQWFVGLSPTVWLSVIWMMWY WGPSLYRILSPFLPLLPIFFCLWVYI

13 of 55

Figure 10: Patient C HBV NT sequence

10	20	30	40	50
CAGCAGCGCCTCCT	CCTGCCTCC	TCCAATCGGCA	GTCAGGAAG	ACAGCCT
60	70	80	90	100
ACTCCCATCTCTCC	ACCTCTAAG	AGACAGTCATC	CTCAGGCCA	TGCAGTG
110	120	130	140	150
GAACTCCAGCACAT	TCCACCAAG	CTCTGCTAGAT	CCCAGAGTG	AGGGGCC
160		180	190	200
TATATTTTCCTGCT		AGTTCCGGAAC	AGTAAACCCT	GTTCCG
210		230	240	250
ACTACTGCCTCTCC		AATCTTCTCGA	GGACTGGGGA	CCCTGC
260	270	280	290	300
ACCGAACATGGAGAG	GCACCACAT	CAGGATTCCTA	GGACCCCTGC	TCGCGT
310 TACAGGCGGGGTTT		330 ACAAGAATCCT		350 CAGAGT
360	370	380	390	400
CTAGACTCGTGGTGG	SACTTCTCT	CAATTTTCTAG	GGGGAACACC	CAAGTG
410	420		440	450
TCCTGGCCAAAATTT	GCAGTCCC		CACTCACCAA	CCTCTT
460 GTCCTCCAATTTGTC	470 CTGGTTATO			500 TTTATC
510	520	530	540	550
ATCTTCCTCTTCATO	CTGCTGCT	ATGCCTCATCT	CCTTGTGGGG	TCTTCT
560	570	580	590	600
GGACTACCAAGGTAT	GTTGCCCGT	TTGTCCTCTAC	CTTCCAGGAA	CATCAA
610 CTACCAGCACGGGAC	620 CATGCAAGA			650 GGAACC
660	670	680	690	700
TCTATGTTTCCCTCT	TGTTGCTGT	ACAAAACCTTC	GGACGGAAA:	TTGCAC

Figure 10

710	720	730	740	750		
TTGTATTCCCAT	CCCATCATCTTG	GGCTTTCGC	AAGATTCCTAT	GGGAGT		
760	770	780	790	800		
GGGCCTCAGTCC	CGTTTCTCCTGGC	TCAGTTTAC	TAGTGCCATTT	GTTCAG		
810	820	830	840	850		
TGGTTCGTAGGG	SCTTTCCCCCACT	GTTTGGCTT	TTAGTTATATG	GATGAT		
860	870	880	890	900		
GTGGTATTGGGG	GCCAAGTCTGTA					
910	920	930	940	950		
TGTTACCAATTT	TCTTTTGTCTTT					
960	970	980	990	1000		
CCAAACGTTGGG	GCTACTCCCTTA					
1010	1020	1030	1040			
TGGGGTACCTTACCACAAGAACATATTGTACACAAAATCAGACAA						

Figure 10 continued

Figure 11: Patient C Polymerase sequence

10	20	30	40	50
EDWGPCTEHGEHHIR	IPRTPARV	TGGVFLVDKNP	HNTTESRLVV	DFSQFS
60 RGNTQVSWPKFAVPN	70 LQSLTNLI	80 SSNLSWLSLDV	90 SAAFYHLPLH	100 IPAAMPH
110	120	130	140	150
LLVGSSGLPRYVARL	SSTSRNIN	YQHGTMQDLHD	SCSRNLYVSI	LLLYKT
160	170	180	190	200
FGRKLHLYSHPIILG	FRKIPMGV	GLSPFLLAQFT	SAICSVVRRA	FPHCLA
210 FSYMDDVVLGAKSVQ	220 HLESLFTA	230 VTNFLLSLGIH	240 LNPTKTKRWG	250 YSLNFM
260 GYVIGSWGTLPQEHI	270 VHKIRQ	-		

Figure 11

16 of 55

Figure 12 Patient C HbsAg sequence

MESTTSGFLGPLLALQAGFFLLTRILTIPQSLDSWWTSLNFLGGTPKCPG QNLQSPTSNHSPTSCPPICPGYRWMCLRRFIIFLFILLLCLIFLWGLLDY QGMLPVCPLLPGTSTTSTGPCKTCTTPAQGTSMFPSCCCTKPSDGNCTCI PIPSSWAFARFLWEWASVRFSWLSLLVPFVQWFVGLSPTVWLLVIWMMWY WGPSLYNXLNPFLPLLPIFFCLWVYI

17 of 55

Figure 13; Patient D NT sequence

10	20	30	40	50
CTCCTGCATC	TACCAATCGGCA	GTCAGGAAG	ACAGCCTACT	CCCATCTCT
60	70	80	90	100
CCACCTCTAA	GAGACAGTCATC		TGCAGTGGAA	CTCCACAAC
				OI OOI IOI MIC
110	120	130	140	150
	GCTCTGCTAGAT		AGGGGCCTCT	₽תיתיתיתית
				militocid
160	170	180	190	200
	CAGTTCCGGGAC	AGTAAACCC	™Ċ₼₼ССС¤ СФ	とりひとりになった。
			TOTTOCOACT	ACIGCCICI
210	220	230	240	250
	CAATCTTCTCGA	GCACTGGGG	~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~	23U 777777777
000:::::::001	0.1110110100A	GGAC1 GGGG	ACCCIGCACI	GAACATGGA
260	270	280	290	200
				300
Oligoliolii()A	ICAGGATTCCTA	GÁNCCCC1G	CICGIGITAC.	AGGCGGTGT
310	320	330	240	250
	320 GACAAGAATCCT		340	350
1111011011	JACAAGAA I CCT	CACAATACC	ACAGAGTCTA	GACTCGTGG
360	270	300	200	
			390	400
IGGACIICIC.	rcaattttctag	GGGAAGCAC	CCGCGTGTCC	I'GGCCAAAA
410	400	420		
410		430		450
TICGCAGTCCC	CCAACCTCCAAT	CACTCACCA	ACCTCTTGTC	CTCCAATTT
4.60	470	400		
460			490	500
GTCCTGGCTAT	CGCTGGATGTG'	rcrgcggcg:	TTTTATCATC:	TTCCTCTTC
510	500			
510				550
ATCCTGCTGCT	PATGCCTCATCT	rcttgttgg:	PTCTTCTGGA:	TACCAAGG
560	570	580	590	600
TATGTTGCCC	STTTGTCCTCTA	CTTCCAGGA	ACGTCAACTA	CCAGCACGG
610	620	630	640	650
GACCATGCAAG	SACCTGCACGAT:	PCCTGCTCA <i>i</i>	AGGAACCTCTA	ATGTTTCCC
660	670	680	690	700
TCATGTTGCT	TACAAAACCTT	CGGACGGAAA	ACTGCACTTGT	TATTCCCAT
			•	
	- 720-	- 730 -		
CCCATCATCCT	'GGGCTTTCGCA			

Figure 13

· 760	770	780	790	800
GTTTCTCTTGACTCAG	TTTACTAGTGC	CATTTGTTC	AGTGGTTCGT	AGGG
810	820		840	850
CTTTCCCCCACTGTTT	GGCTTTCAGTT	ATATGGATGA	ATGTGGTATTC	GGG
860	870	880	890	900
GCCAAGTCTGTACAAC	ATCTTGAGTCC	CTTTATACC	CTATTACCA?	TTT
910	920	930	940	950
TCTTTTGTCTTTGGGT	ATACATTTAAA	CCCTAATAAA	ACCAAGCGAT	'GGG
960	970	980		.000
GTTACTCCCTTAACTT	CATGGGATATG	TCATTGGAAG	TTGGGGGACT	'TTA
	1020			
CCACAGGAACATATTG	IGCTC			

Figure 13 continued

19 of 55

Figure 14: patient D HBV POL sequence

EDWGPCTEHGEHNIRIPRTPARVTGGVFLVDKNPHNTTESRLVVDFSQFS ${\tt RGSTRVSWPKFAVPNLQSLTNLLSSNLSWLSLDVSAAFYHLPLHPAAMPH}$ LLVGSSGLPRYVARLSSTSRNVNYQHGTMQDLHDSCSRNLYVSLMLLYKT FGRKLHLYSHPIILGFRKIPMGVGLSPFLLTQFTSAICSVVRRAFPHCLA FSYMDDVVLGAKSVQHLESLYTAITNFLLSLGIHLNPNKTKRWGYSLNFM GYVIGSWGTLPQEHIVL

20 of 55

Figure 15 Patient D HBsAg sequence

MESTTSGFLGPLLVLQAVFFLLTRILTIPQSLDSWWTSLNFLGEAPACPG QNSQSPTSNHSPTSCPPICPGYRWMCLRRFIIFLFILLLCLIFLLVLLDY QGMLPVCPLLPGTSTTSTGPCKTCTIPAQGTSMFPSCCCTKPSDGNCTCI PIPSSWAFARFLWEWASVRFS*LSLLVPFVQWFVGLSPTVWLSVIWMMWY WGPSLYNILSPFIPLLPIFFCLWVYI

21 of 55

Figure :	16:	Patient	E	HBV	nt	sequence
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rigure	Tp:	Patien	it E	нву	nt	seq	ience			
	10		20			30		40		50
AGTCATO	CCTCA	GGCCAT	'GCA	STGG	AACI	CCAG	CACA	TCCA	CCAAG	CTCT
	60		70			80		90		100
GCTAGAT	CCCA	GAGTGA	GGGG	SCCTA	ATAC	TTTC	CTGCT	GGTG	GCTCC	\GTT
	110		120		1	30		140		1 = 0
CAGGAAC						TGCC	TCTCC	CATA	TCGTC	ATC
TTĊTCGA		тессер	170	יכפאפ	1	.80 	100x0x	190	03 03 mc	200
1101001	.00110	100001		GCAC	JUGA	MINI	GGAGA	IGCAC	CACATO	AGG
	210		220		2	30		240		250
ATTCCTA	GGAC	CCCTGC	TCGI	GTT	ACAG	GCGG	GGTTI	TTCT	TGTTGF	CAA
	260		270		2	80		290		300
GAATCCT	CACA	ATACCA	CAGA	GTCI	AGA	CTCG	TGGTG	GACT	TCTCTC	:AAT
	310		320		2	30		240		250
TTTCTAG		AGCACC	CGCG	TGTC	CTG	GCCA	AAATT	340 'TGCA	GTCCCC	350 3AC
		ሮክ ሮመል አ	370 CCDC	mmen	3	80		390		400
CTCCAAT	CACI	CACIAA	CCIC	1161	CCT	CCAA	TTTGT	CCTG	GTTATC	GCT
			420		4	30		440		450
GGATGTG	TCTG	CGGCGT	TTTA	TCAT	'CTT	CCTC	TTCAT	CCTG	CTGCTA	TGC
	460		470		4	80		490		500
CTCATCT	TCTT	GTTGGT'	TCTT	CTGG	ACT	ACCA	AGGTA	TGTT	GCCCGT	TTG
	510		E 2 0		_	20		540		
TCCTCTA	CTTC	: CAGGAA	OZU CATC	ААСТ	DOA'	3U AGCA	CGGGA	540 CCAT(3C	550 CCT
										001
	560 maama		570	~~~	5	80		590		600
GCACGAC'	TCCT	SCTCAA	3GAA	CCTC	TAT	GTTT	CCCTC	TTGT'	rgttgt	ACA
	610	(620		6	30		640		650
AAACCTT	CGGA	CGGAAA!	rtgc.	ACTT	GTA'	TTCC	CATCC	CATC	ATCTTG	GGC
	660	(570		6	80		690		700
TTTCGCA	AGATT	CCTAT	GGA	GTGG	GCC:	TCAG'	TCCGT'	TTCT	CATGGC	TCA

22 of 55

710	720	730	740	750
GTTTACTAGTGCCATT	TTGTTCAGTGG	TTCGTAGGGC	TTTCCCCCAC	TGTT
760	770	780	790	800
TGGTTTTCAGTTATGT	GGATGATGTG	GTATTGGGGG	CCAAGTCTGC	ACAA
810	820	830	840	850
CATCTTGAATCCCTTT	TTACCGCTAT	TACCAATTTT	CTTTTGTCTT	TGGG
860	870	880	890	900
TATACATTTAAACCMT	AATAAAACCA	AACGTTGGGG	CTATTCCCTT	AACT
910	920	930	940	950
TTATGGGATATGGAAT	TGGAAGTTGG	GGTCCTGCCC	AGGGAAGATG	
				- 0
GGG				

Figure 16 continued

23 of 55

Figure 17 Patient E: HBV polymerase

20 30 ${\tt SSSGHAVELQHIPPSSARSQSEGPILSCWWLQFRNSKPCSDYCLSHIVNL}$ 70 80 . 90 ${\tt LEDWGPCTEYGEHHIRIPRTPARVTGGVFLVDKNPHNTTESRLVVDFSQF}$ 130 140 SRGSTRVSWPKFAVPNLQSLTNLLSSNLSWLSLDVSAAFYHLPLHPAAMP 190 170 180 HLLVGSSGLPRYVARLSSTSRNINYQHGTMQDLHDSCSRNLYVSLLLLYK 220 230 240 TFGRKLHLYSHPIILGFRKIPMGVGLSPFLMAQFTSAICSVVRRAFPHCL 260 270 280 290 VFSYVDDVVLGAKSAQHLESLFTAITNFLLSLGIHLNXNKTKRWGYSLNF MGYGIGSWG

24 of 55

Figure 18: Patient E HBsAg

	10	20	30	40	50
QPTPI	SPPLRDSHPQ	AMQWNSST	FHQALLDPRVR	GLYFPAGGS	SSGTVNP
	60	70	80	90	100
VPTT	SPISSIFSRI	GDPAPNME	STTSGFLGPLL	VLQAGFFLLI	RILTIP
	110	120	130	140	150
QSLDS	WWTSLNFLGG	APACPGQN1	LQSPTSNHSLT	SCPPICPGYF	RWMCLRR
	160	170	180	190	200
FIIFI	FILLLCLIFI	LVLLDYQGI	4LPVCPLLPGT	STTSTGPCKT	
	210	220	230	240	250
GTSME	PSCCCTKPSD	GNCTCIPI	PSSWAFARFLW	EWASVRFSWI	
	260	270	280	290	300
VQWFV	GLSPTVWFSV	MWMMWYWG	SLHNILNPFL		
IKPNV	GA				

25 of 55

Figure 19: Patient F: nt sequence

Figure	19:	Patient	F:	nt	sequence		
	10		20		30	40	50
CCAATO	CGGC	AGTCAGGA	AGAC	CAGC	CTACTCCC.	ATCTCTCCACC	TCTAAGA
	60		70		80	90	100
GACAGI	CATO	CTCAGGC	CATO	CAG	STGGAACTC	CAGCACATTCC	ACCAAGC
	110		120		130	140	150
TCTGCT	'AGA'I	CCCAGAG'	rga(GGG	CCTATACT'	PTCCTGCTGGT	GGCTCCA
	160)	170		180	190	200
GTTCCG	GAAC	CAGTAAAC	CCTG	TTC	CGACTACT	GCCTCTCCCAT.	ATCGTCA
» m c m m c	210		220		230	240	250
ATCTTC	TCGA	AGGACTGG(GGAC	CCT	'GCACCGAA'	PATGGAGAGCA	CCACATC
A C C A D D	260	CORCOCO	270		280	290	300
AGGATT	CCTA	IGGACCCC.	rgci	CGT	'GTTACAGG(CGGGGTTTTTC	ITGTTGA
CAACAA	310		320	יה הי	330	340	350
CAAGAA	11001					CGTGGTGGAC'	
<u>አ</u> አጥጥጥ ተ	360 כתאם		370	1 N C C	380	390 CCAAAATTTGC	400
WIIII	CIAG						
AACCTC	410	· የርልርሞርልርር	120	CTC	430	440 CAATTTGTCCT	450
1110010							
GCTGGA	460 TGTG	YCTGCGGC	170 :Стт	ጥጥΔ	480 ጥር አጥር ጥጥር ር	490 CTCTTCATCCT	500
TGCCTC		5 TCTTGTTC	520 GTT	СТТ	530 CTGGACTAC	540 CAAGGTATGT	
TTGTCC	560 TCTA				580 AACTACCAG	590 GCACGGGACCAT	600 GCAAGA
CCTGCA	610 CGAC	-			630 CCTCTATGT	640 TTCCCTCTTGT	650 TGCTGT

660	670	680	690	700
ACAAAACCTTCGGAC	GGAAATI	GCACTTGTATTC	CCATCCCAT	CATCTTG
710	720	730	740	750
GGCTTTCGCAAGATT	CCTATGO	GAGTGGGCCTCA	GTCCGTTTC'	TCCTGGC
760	770	780	790	800
TCAGTTTACTAGTGC	CATTTGT	TCAGTGGTTCGT	AGGGCTTTC	
810	820	830	840	850
GTTTGGCTTTCAGTT	ATATGGA	TGATGTGGTATT	GGGGCCAA	STCTGTA
860	870	880	890	900
CAACATCTTGAATCC	CTTTTTA	CCGCTGTTACCA	ATTTTCTTT	FGTCTTT
910	920	930	940	950
GGGTATACATTTAAA	CCCTACT	'AAAACTAAACGT'	GGGGCTAC:	CCCTTA
960	970	980		
ACTTCATGGGATATG	PAATTGG	AAGTTGGGGTAC	CTTG	

Figure 19 continued

27 of 55

Figure 20 Patient F Pol Amino acid sequence

10	20	30	40	50
EDWGPCTEYGEHHI	RIPRTPARVI	GGVFLVDKNE	HNTTESRLVV	DFSQFS
60	70	80	90	100
RGSTHVSWPKFAVE	NLOSLINLLS	SSNLSWLSLDV	'SAAFYHLPLH	PAAMPH
110	120	130	140	150
LLVGSSGLPRYVAR	RLSSTSRNINY	QHGTMQDLHC	SCSRNLYVSL	LLLYKT
160	170	180	190	200
FGRKLHLYSHPIII	GFRKIPMGVO	LSPFLLAQFT	'SAICSVVRRA	FPHCLA
210	220	230	240 .	250
FSYMDDVVLGAKSV	QHLESLFTAV	TNFLLSLGIH	LNPTKTKRWG	YSLNFM
CVIITCORG				
GYVIGSWG				

28 of 55

Figure 21 Patient F HBsAg seq

MESTTSGFLGPLLVLQAGFFLLTRILTIPQSLDSWWTSLNFLGGAPTCPG QNLQSPTSNHSPTSCPPICPGYRWMCLRRFIIFLFILLLCLIFLLVLLDY QGMLPVCPLLPGTSTTSTGPCKTCTTPAQGTSMFPSCCCTKPSDGNCTCI PIPSSWAFARFLWEWASVRFSWLSLLVPFVQWFVGLSPTVWLSVIWMMWY WGPSLYNILNPFLPLLPIFFCLWVYI

29 of 55

Figure 22: Patient G ; HBV nt

Figure	22:	Patient	t G	; HBV	nt			
TCCCC	1(20) >	3	0	40	50
10000	CICC.	GCCTCCZ	ACC.	MICG	CAGT	CAGGAA	GCAAC	CTACCCCGC
ጥርጥር ጥ/	60		70) יא כיייט	8	0	90	100
10101	COACC	, I I I GAG	MU	MOICE	AICCI	CAGGCCC	oTGCAG	IGGAACTCC
	110)	120)	13	0	140	150
ACAAC	CTTCC	CACCAAA	CTCI	rgcaa	GATCC	CAGAGTO	SAGGGG	CCTGTATCT
	160		170)	18	0	190	200
CCCTG	CTGGI	GGCTCC	AGTI	'CAGG	AACAG	CAAACCC	CTGTTC	CGACTACTG
	210		220)	23	0	240	250
CCTCTC	CGCTI	ATCGTC	ATC	CTTCT	CGAGG	ATTGGGG	SACCCT	GCGCTGAAC
	260)	270)	280	ס	290	300
ATGGAC	SAACA	TCACATO	AGG	ACTC	CTAGG	ACCCCTT	CTCGT	STTACAGGC
	310	1	320)	33/)	340	350
GGGGT			CAA	GAATO	CTCA	CAATACO	CGCAGA	350 TCTAGACT
CGTGGT	360 GGAC) :GAACTA		400 GTCTTGGC
~~~~~~	410		420		430	) 	440	450
CAAAA1	TCGC	GGTCCCC	AAC	CTCCA	AATCAC	CTCACCA	ACCTC	CTGTCCTCC
	460		470		480	)	490	500
GACTTO	STCCT	GGTTATC	GCT	GGATG	TATCI	rgcggcg	TTTTAT	CATATTCC
			520		530	)	540	550
TCTTCA	TCCT	GCTGCTA	TGC	CTCAT	CTTCI	TGTTGG	TTCTTC	CTGGACTAT
	560		570		580	)	590	600
CAAGGT	'ATGT	TGCCCGT	TTG	TCCTC	TAAT	CCAGGA	TCCTC	ACCACCAG
	610		620		630	)	640	650
CACGGG								CTCTATGT
	660					)		
ATCCCT		TTGCTGT	ACC.	AAACC	TTCG	, BACGGAA	690 ATTGCA	700 CCTGTATT

710	720	730	740	750	
CCCATCCCATCAT	CTTGGGCTTT	CGGAAAATTC	CTATGGGAGT		
				5555515	
760	770	780	790	800	
AGCCCGTTTCTCC	_				
	TOGOTONGIT	INCINGIGCC	ATTIGITORG.	regrice	
810	820	920	0.40	050	
			840	850	
TAGGGCTTTCCCC	CACTGTTTGG	CTTTCAGTTAI	CATGGATGAT	GTGGTAT	
860	870	880	890	900	
TGGGGGCCAAGTC	IGTACAGCAT(	CTTGAGTCCCT	TTTTACCGC	TGTTACC	
910	920	930	940	950	
AATTTTCTTTTGT					
	J11100011111	CATTIANCO	CIAACAAAA	JAAAGAG	
960	970	000	000	1000	
		980	990	1000	
ATGGGGTTACTCT	JTAAATTTTA!	rgggctatgtc	ATTGGAAGTT	PATGGGT	
1010		1030	1040		
CCTTGCCACAAGAACACATTATACTAAAAATCAAAGATTGTTT					

Figure 22 continued

### 31 of 55

Figure 23 Patient G HBV POL

20 30 EDWGPCAEHGEHHIRTPRTPSRVTGGVFLVDKNPHNTAESRLVVDFSQFS 70 80 RGNYRVSWPKFAVPNLQSLTNLLSSDLSWLSLDVSAAFYHIPLHPAAMPH 120 130  ${\tt LLVGSSGLSRYVARLSSNSRILNHQHGNMPNLHDSCSRNLYVSLLLLYQT}$ 170 180 FGRKLHLYSHPIILGFRKIPMGVGLSPFLLAQFTSAICSVVRRAFPHCLA 220 230 240 FSYMDDVVLGAKSVQHLEŞLFTAVTNFLLSLGIHLTPNKTKRWGYSLNFM GYVIGSYG

### 32 of 55

Figure 24: Patient G HbsAg

20 30 MENITSGLLGPLLVLQAGFFLLTRILTIPQSLDSWWTSLSFLGGTTVCLG 70 80 90 QNSRSPTSNHSPTSCPPTCPGYRWMYLRRFIIFLFILLLCLIFLLVLLDY 120 130 QGMLPVCPLIPGSSTTSTGTCRTCTTPAQGTSMYPSCCCTKPSDGNCTCI 170 180 190 PIPSSWAFGKFLWEWASARFSWLSLLVPFVQWFVGLSPTVWLSVIWMMWY 220 WGPSLYSILSPFLPLLPIFFCLWVYI

# 33 of 55

## Figure 25 Patient H nt seq

10	20	30	40	50
CGCCTCCTGCC	TCCACCAATCGCC	AGTCAGGAA	GGCAGCCGACC	CCCACTG
60	70	80	90	100
TCTCCACCTTT	GAGAGACACTCAT	CCTCAGGCC	GTGCAGTGGA <i>I</i>	ACTCCAC
110	120	130	140	150
AACCTTCCACC	AAACTCTGCAAGA	TCCCAGAGT	GAGAGGCCTGT	CATTTCC
160	170		190	200
CTGCTGGTGGC	TCCAGTTCAGGAA		CTGTTCCGACO	CACTGCC
	220 GTCAATCTTCTCG		240 SACCCTGCGCT	250 GAACAT
260	270	280	290	300
GGAGAACATCA	CATCAGGATTCCT	AGGACCCCTI	CCTCGTGTTAC	AGGCGG
310	320	330		350
GGTTTTTCTTG	ITGACAAGAATCC	TCACAATACO		GACTCG
	370 ICTCAGTTTTCTA	380 GGGGAAACC <i>I</i>		400 TGGCCA
410	. 420	430	440	450
AAATTCGCAGTO	CCCCAACCTCCAA	TCACTCACC <i>A</i>	ACCTCCTGTC	CTCCAA
460 CTTGTCCTGGTT	470 FATCGCTGGATGT	480 GTCTGCGGCG		
510	520		540	550
TTCATCCTGCTC	SCTATGCCTCATC		TTCTTCTGGA	CTATCA
560	570		590	600
AGGTATGTTGCO	CCGTTTGTCCTCT		TCCTCAACCA	CCAGCA
610 CGGGACCATGCO	620 CGAACCTGCACGA			
660 CCCTCCTGTTGC	670 CTGTACCAAACCT			700 TATTCC

Figure 25

710	720	730	740	750
CATCCCATCATCTTG	GGCTTTC	GCAAAATTCCTA	TGGGAGTGG	GGCTCAG
760			790	800
CCCGTTTCTCATGGC	TCAGTTT	ACTAGTGCCATT'	TGTTCAGTG	GTTCGTA
810		830	840	850
GGGCTTTCCCCCACT	GTTTGGC'	TTTCAGTTATGT(	GGATGATGT(	GGTAŢTG
860			890	900
GGGGCCAAGTCTGTA	TCGCATC!	rtgagtcccttt:	TTACCGCTG1	TACCAA
910	920		940	950
TTTTCTTTTGTCTTT	GGGTATA	CATTTAAACCCT	AACAAAACG	AAAAGAT
		980	990	1000
GGGGTTACTCTTTAA	ATTTTATO	GGGTATGTTAT:	rggatgttai	rGGGTCC
1010	1020			
TTGCCACAAGAACAC	ATCGTAC	\AAAA		

Figure 25 continued

PCT/AU2004/001440

#### 35 of 55

Figure 26: Patient H HBV pol

20 30 40 EDWGPCAEHGEHHIRIPRTPSRVTGGVFLVDKNPHNTAESRLVVDFSQFS 80 90 RGNHRVSWPKFAVPNLQSLTNLLSSNLSWLSLDVSAAFYHIPLHPAAMPH 120 130 140 LLVGSSGLSRYVARLSSNSRILNHQHGTMPNLHDSCSRNLYVSLLLLYQT 170 180 190  ${\tt FGRKLHLYSHPIILGFRKIPMGVGLSPFLMAQFTSAICSVVRRAFPHCLA}$ 220 230 240  ${\tt FSYVDDVVLGAKSVSHLESLFTAVTNFLLSLGIHLNPNKTKRWGYSLNFM}$ GYVIGCYGSLPQEH

#### 36 of 55

Figure 27: Patient H HBsAg

20 30 40 MENITSGFLGPLLVLQAGFFLLTRILTIPQSLDSWWTSLSFLGETTVCLG 70 80 QNSQSPTSNHSPTSCPPTCPGYRWMCLRRFIIFLFILLLCLIFLLVLLDY 120 130 QGMLPVCPLIPGSSTTSTGPCRTCTTPAQGTSMYPSCCCTKPSDGNCTCI 170 180 190 200 PIPSSWAFAKFLWEWGSARFSWLSLLVPFVQWFVGLSPTVWLSVMWMMWY 220 WGPSLYRILSPFLPLLPIFFCLWVYI

Figure 28 Patient I HBV nt seq

rigure	28	Patient	: I	нву	nt	seq				
CAACTTO	10 STCC	) CTGGTTAT	20 CG0	) CTGG2	ATGI	30 GTCT	GCGGCG	40 STTTT	'ATCAT	50 ATTC
CTCTTC	60 ATCC	) CTGCTGCT	7( ATC	) SCCT(	CATO	80 CTTC1	TGTTGC	90 STTCT	'TCTGG	100 ACTA
	110		120	)		130		140		150
	160		170	)		180		190		200
	210		220	)		230		240		250
	260	TCATCCI	270	)		280		290		300
	310	)	320	)		330		340		350
CAGCCCG	360	1	370	)		380		390		400
GTAGGGC	410	1	420	)		430		440		450
TTGGGGG	3CCA 460									
CAATTTI	CTT 510	TTGTCTC	TGG	GTAT	CACA	TTTA	AACCCT	CACA	AAACA	AAAA
GATGGGG			CAI	TTC	ATGG	GCTA	TGTCAT	CGGA	TGTTA!	rggg

TCTTTGCCAC

Figure 28

## 38 of 55

Figure 29 Patient I HBV pol

NLSWLSLDVSAAFYHIPLHPAAMPHLLVGSSGLSRYVARLSSTSRIFNHQ  ${\tt HGSMQNLHDSCSRNLYVSLMLLYQTFGRKLHLYSHPIILGFRKIPMGVGL}$  ${\tt SPFLMAQFTSAICSVVRRAFPHCLAFSYVDDVVLGAKSVSHLESLFTAVT}$ NFLLSLGIHLNPHKTKRWGYSLHFMGYVIGCYGSLP

## 39 of 55

Figure 30 Patient I: HBsAg

10 20 30 40 50
TCPGYRWMCLRRFIIFLFILLLCLIFLLVLLDYRGMLPVCPLLPGSSTTS

60 70 80 90 100
TGPCRTCTTPAQGTSMYPSCCCTKPSDGNCTCIPIPSSWAFGKFLWEWAS

110 120 130 140 150
ARFSWLSLLVPFVQWFVGLSPIVWLSVMWMMWYWGPSLYRILSPFLPLLP

160 170 180
IFFCLWVYI*

#### 40 of 55

Figure 31

710		730		750
CCCATCCCATCAT	CTTGGGCTTT	CGCAAGATTC	CTATGGGAGT	GGCCTC
760	770	780	790	800
AGTCCGTTTCTCC	TGGCTCAGTT	TACTAGTGCC	ATTTGTTCAG	
810		830		850
TAGGGCTTTCCCC	CACTGTTTGG	CTTTCAGTTA	PATGGATGAT	STGGTAT
860	870	880	890	900
TGGGGGCCAAGTC	TGTACAACATO	CTTGAATCCCT	TTTTACCGC	GTTACC
222				
			940	950
AATTTTCTTTTGT	'CTTTGGGTAT <i>A</i>	CATTTAAAC	CCTACTAAAA	CTAAACG
0.50	07.0			
		980	990	1000
TTGGGGCTACTCC	CTTAACTTCAT	GGGATATGT	AATTGGAAGT1	GGGGTA
1010	1020			
CCTTACCACAGGA		CACAAA		

Figure 31 continued

Figure 32 Patient J HBV pol

10 20 30 40 50
EDWGPCTEYGEHNIRIPRTPARVTGGVFLVDKNPHNTTESRLVVDFSQFS

60 70 80 90 100
RGSTHVSWPKFAVPNLQSLTNLLSSNLSWLSLDVSAAFYHLPLHPAAMPH

110 120 130 140 150
LLVGSSGLPRYVARLSSTSRNINYQHGTMQDLHDSCSRNLYVSLLLLYKT

160 170 180 190 200
FGRKLHLYSHPIILGFRKIPMGVGLSPFLLAQFTSAICSVVRRAFPHCLA

210 220 230 240 250 FSYMDDVVLGAKSVQHLESLFTAVTNFLLSLGIHLNPTKTKRWGYSLNFM

260 GYVIGSWGTLPQEHIVHK

### 43 of 55

Figure 33. Patient J HBsAg

10 20 30 40 50 MESTTSGFLGPLLVLQAGFFLLTRILTIPQSLDSWWTSLNFLGGAPTCPG

60 70 80 90 100 QNLQSPTSNHSPTSCPPICPGYRWMCLRRFIIFLFILLLCLIFLXVLLDY

110 120 130 140 150 QGMLPVCPLLPGTSTTSTGPCKTCTIPAQGTSMFPSCCCTKPSDGNCTCI

160 170 180 190 200 PIPSSWAFARFLWEWASVRFSWLSLLVPFVQWFVGLSPTVWLSVIWMMWY

210 220 WGPSLYNILNPFLPLLPIFFCLWVYI

Figure 33

## 44 of 55

Figure 34 Patient K HBV nt

rigure 34	Patient	K HBV Dt			
Om o om o om	10	20	30	40	50
CTCCTCCT	rGCCTCCAC	CAATCGGCA	GTCAGGAAGA	CAGCCTACACC	CATC
	60	70 ·	80	90	100
TCTCCACC	TCTAAGAGA	ACAGTCATC	CTCAGGCCAT	GCAGTGGAACT	CCAG
1	.10	120	130	140	150
CACATTCC	CACCAAGCT	CTGCTAGAT	CCCAGAGTGA	GGGCCTATAC	TTTC
1	.60	170	180	190	200
CTGCTGGT	GGCTCCAG	TTCAGGAAC	AGTAAACCCT	GTTCCGACTAC	TGCC
2	:10	220	230	240	250
		CTTCTCGA	GGACTGGGGA	CCTGCACCGA	ATAT
2	:60	270	280	290	300
		GATTCCTA	GGACCCCTGCT	CGTGTTACAG	GCGG
2	10	220	330	240	252
		AGAATCCT(	330 CACAATACCAC	340 CAGAGTCTAGA	350 CTCG
		370 ATTTTCTAGO	380 GGGGAGCACCO	390 CACGTGTCCTG	400
	10 ACTCCCCAA	420 CCTCCNNTC	430	440 CTCTTGTCCT	450
	1101000011				CCAA
	60	470		490	500
TITGICCI	GGITAICGC	TGGATGTG	rcrgcggcgri	TTATCATCTT	CCTC
	10	520	530	540	
TTCATCCT	GCTGCTATG	CCTCATCT	CTTGTTGGTI	CTTCTGGACT	ACCA
		570	580	590	600
AGGTATGT	TGCCCGTTT	GTCCTCTAC	CTTCCAGGAAC	ATCAACTACC	AGCA
	10	620	630	640	650
CGGGACCA'	TGCAAGACC	TGCACGATI	CCTGCTCAAG	GAACCTCTAT	GTTT
_			680		700
CCCTCTTG	TTGCTGTAC	AAAACCTTC	GGACGGAAAT	TGCACTTGTA	TTCC

Figure 34

## 45 of 55

7	10	720	730	740	750	
CATCCCAT	CATCTTGGG	CTTTCGCAAC	SATTCCTATGO	GAGTGGGCC	TCAG	
	60	770			800	
TCCGTTTC	CTCCTGGCTC	CAGTTTACTAC	GTGCCATTTGI	TTCAGTGGTT	CGTA	
8	310	820	830	840	850	
GGGCTTTC	CCCCACTG	TTTGGCTTTC	AGTTATATGG?	ATGATGTGGT	ATTG	
8	360	870	880	890	900	
GGGGCCAA	GTCTGTACA		ATCCCTTTTTA	ACCGCTGTTA	CCAA	
g	910	920	930	940	950	
TTTTCTTI	TGTCTTTG		PAAACCCTRC	PAAAACCAAA	CGTT	
9	960	970	980	990	1000	
GGGGTTACTCCCTTAACTTCATGGGATATGTAATTGGAAGTTGGGGTACC						
.10	010	1020	1030			
TTACCACA	AGGAACATA:	TTGTACACAA	AATCAAACA			

Figure 34 continued

#### 46 of 55

Figure 35 Patient K HBV pol

20 30 SSCLHOSAVRKTAYTHLSTSKRQSSSGHAVELQHIPPSSARSQSEGPILS 80 CWWLQFRNSKPCSDYCLSHIVNLLEDWGPCTEYGEHHIRIPRTPARVTGG 130 VFLVDKNPHNTTESRLVVDFSQFSRGSTHVSWPKFAVPNLQSLTNLLSSN 170 180 LSWLSLDVSAAFYHLPLHPAAMPHLLVGSSGLPRYVARLSSTSRNINYQH 220 230 GTMQDLHDSCSRNLYVSLLLLYKTFGRKLHLYSHPIILGFRKIPMGVGLS 270 280 PFLLAQFTSAICSVVRRAFPHCLAFSYMDDVVLGAKSVQHLESLFTAVTN 320 330 FLLSLGIHLNPXKTKRWGYSLNFMGYVIGSWGTLPQEHIVHKIK

## 47 of 55

Figure 36 Patient K HbsAg

יוואים מיות'	10			40 QALLDPRVRGI	50 .VEP	
PPASINE	(Ö2GVÖLILT)	SEEPHOOUE OF	TIONIADOLLIN	SUMPOLICATION	1111	
	60	70	80	90	100	
AGGSSSG	STVNPVPTTAS	SPISSIFSKI	PDPAPNMEST	rsgflgpllvi	υQAG	
	110		130		150	
FFLLTR	[LTIPQSLDSV	WTSLNFLGGA	451.C5GOUTO	SPTSNHSPTSO	SPPI	
	160	170	180	190	200	
CPGYRWN	CLERFITFI			PVCPLLPGTST	TST	
010111111	TODICICE PED D.					
	210	220	230	240	250	
GPCKTC:	ripaqgtsmfi	PSCCCTKPSD	GNCTCIPIPS	SWAFARFLWE	VASV	
	260	270	280	290	300	
RFSWLSLLVPFVQWFVGLSPTVWLSVIWMMWYWGPSLYNILNPFLPLLPI						
	310		330			
FFCLWV	YI*TLLKPNV	GVTPLTSWDM	*LEVGVPYHR	NILYTKSN		

Figure 36

### 48 of 55

Figure 37 Patient L HBV nt

10 CAGTCCGGAAG	20	30	40	50 ACACTCA
CAGICCGGAAGG	CAGCCIACICC	CITATCICCA	CICIAAGGG	MCACICA
60		80		100
TCCTCAGGCCAT	TGCAGTGGAACT	CCACCACTTT	CATCAAACT	CTTCAAG
110		130		150
ATCCCAGAGTC	AGGGCTCTGTAC	TTTCCTGCTG	GTGGCTCCAG	TTCAGGA
160	170	180	190	200
ACAGTGAGCCCT	GCTCAGAATAC	TGCCTCTGCC	ATATCGTCAA	CCTTCTC
210	220	230	240	250
GAAGACTGGGG	ACCCTGTACCGA	ACATGGAGAA	CATCGCATCA	GGACTCC
260	270	280	290	300
TAGGACCCCTGC	CTCGCGTTACAG	GCGGGGTTTT	CTCGTTGAC	AAAAATC
310	320	330	340	350
CTCACAATACCA				
010110111111001	1011011010111101	01001001001	10110101011	21111101
360	370	380	300	400
AGGGGGAACAC				
NOGOGGANCACC	CGIGIGICIIC	GCCAAAA11C	CAGICCCAA	AICICCA
410	420	430	440	450
GTCACTCACCA				
GICACTCACCA	CTIGTTGTCCT	CCAATTTGTC	LIGGITATCG	CTGGATG
460	470	480	400	F00
TGTCTGCGGCGT	TTTATCATCTI	CCTCTGCATC	STECTECTAT	GCCTCAT
		530		
CTTCTTGTTGGT	TCTTCTGGACT	'ATCAAGGTAT	STTGCCCGTT	TGTCCTC
• •		580		
TAATTCCAGGAT	CATCAACCACC	AGCACCGGAC	CATGCAGAAC	CTGCACG
		630		
ACTCCTGCTCAF	AGGAACCTCTAT	GTTTCCCTCAT	<b>IGTTGCTGT</b> À	CAAAACC

660	670	680	690	700
TACGGACGGAAACTG	CACCTGTATT	CCCATCCCAT	CATCTTGGG	CTTTCG
710	720			750
CAAAATACCTATGGG	AGTGGGCCTC	AGTCCGTTTC	TCTTGGCTC	CAGTTTA
760	770	780	790	800
CTAGTGCCGTTTGTTC	CAGTGGTTCG	TAGGGCTTTC	CCCCACTGI	CTGGCT
810	820	830	840	850
TTCAGTTATATGGAT	SATGTGGTAT	TGGGGGCCAA	GTCTGTACA	AACATCT
860	870	880	890	900
TGAGTCCCTTTATGC	CGCTGTTACC	AATTTTCTTT	TGTCTTTG	GTATAC
910	920	930	940	950
ATTTAAACCCTCACA	AAACAAAAAG	ATGGGGATAT	TCCCTTCA	ATTCATG
960	970	980		
GGATATGTAATTGGG	GGTTGGGGCT	CCTTG		

Figure 37 continued

#### 50 of 55

Figure 38. Patient L Pol

10 20 30 40 50

EDWGPCTEHGEHRIRTPRTPARVTGGVFLVDKNPHNTTESRLVVDFSQFS

60 70 80 90 100

RGNTRVSWPKFAVPNLQSLTNLLSSNLSWLSLDVSAAFYHLPLHPAAMPH

110 120 130 140 150

LLVGSSGLSRYVARLSSNSRIINHQHRTMQNLHDSCSRNLYVSLMLLYKT

160 170 180 190 200

YGRKLHLYSHPIILGFRKIPMGVGLSPFLLAQFTSAVCSVVRRAFPHCLA

210 220 230 240 250

FSYMDDVVLGAKSVQHLESLYAAVTNFLLSLGIHLNPHKTKRWGYSLQFM

GYVIGGWG

### 51 of 55

Figure 39 Patient L HBsAg

10 20 30 40 50

MENIASGLIGPLIALQAGFFSLTKILTIPQSLDSWWTSLNFLGGTPVCLG

60 70 80 90 100

QNSQSQISSHSPTCCPPICPGYRWMCLRRFIIFLCILLLCLIFLLVLLDY

110 120 130 140 150

QGMLPVCPLIPGSSTTSTGPCRTCTTPAQGTSMFPSCCCTKPTDGNCTCI

160 170 180 190 200

PIPSSWAFAKYLWEWASVRFSWLSLLVPFVQWFVGLSPTVWLSVIWMMWY

210 220

WGPSLYNILSPFMPLLPIFFCLWVYI

#### 52 of 55

## 53 of 55

10 20 30 40 50
CWWLQFRNSKPCSDYCLSLIVNLLEDWGPCAEHGEHHIRIPRTPSRVTGG

60 70 80 90 100
VFLVDKNPHNTAESRLVVDFSQFSRGNYRVSWPKFAVPNLQSLTNLLSSN

110 120 130 140 150
LSWLSLDVSAAFYHXPLHPAAMPHLLVGSSGLSRYVARLSSNSRILXHQH

160 170 180 190 200
GTMPNLHDYCSRNLYVSLLLLYQTYGRKLHLYSHPILGFRKIPMGVGLS

210 220 230 240 250
PFLLAQFTSAICSVVRRAFPHCLAFSYMDDVVLGAKSVXHLESLFTAVTN

260 270 280 290
FLLSLGIHLNPNKTKRWGYSLNFMGYVIGSYGSLPQEHIIQKIKECFRK

## Figure 41

20 30 40 PAGGSSSGTVNPVPTTASPLSSIFSRIGDPALNMENITSGFLGPLLVLQA 70 80 90 GFFLLTRILTIPQSLDSWWTSLNFRGGTTVCLGQNSQSPTSNHSPTSCPP 130 120 140 TCPGYRWMCLRRFIIFLFILLLCLIFLLVLLDYXGMLPVCPLIPGSSXTS 180 170 190 TGPCRTCMTTAQGTSMYPSCCCTKPTDGNCTCIPIPSSWAFGKFLWEWAS 230 220 240 ARFSWLSLLVPFVQWFVGLSPTVWLSVIWMMWYWGPSLYXILSPFLPLLP 260 IFFCLWVYI*

Figure 42

# 54 of 55

	10			40	50
CTTTCAC	CCAAACTCTGC	CAAGATCCCC	CTGCTGGTGG	CTCCAGTTCA	GGAA
CACMAA	60 \CCC#C##CCC	70			100
CAGTAA	30001611000	SACTACTECC	rerecertar	CGTCAATCTT	CTCG
<b>አ</b> ርርልጥጥ(	110	120	130	140 ACATCAGGAT	150
MOOMITC	30000000100			noni ondoni .	1001
AGGACCO	160 ************************************	170	180 בפיייייייייייייייייייייייייייייייייייי	190 GTTGACAAGA	200
NOONCCC					AICC
тсасаал	210	220 "כידאפאכידיכפי	230 PGGTGGACTT	240 CTCTCAATTT	250
10110/111				CICIONALLI	ICIA
GGGGGA	260 \CTACCGTGTG	270 בערעענגריים	280 ••••••••••••••••••••••••••••••••••••	290 ICCCCAACCT	300
GGGGA	OIACCOIGIC	31C11GGCCA2	AMII COCAG	ICCCCAACCI	CCAA
<b>ጥ</b> ሮ እ ሮሞሮ ፣	310 \CCAACCTCCT	320 פרובים אורים א	330	340 TTATCGCTGG	350
TOACTOR	CCAACCICCI	GICCICCAM	2116166166	ITAICGCIGG	HIGI
CTCTCCC	360	370	380	390 IGCTATGCCT	400
GICIGC	GCGITITALC	MICTICCIC.	PICATOCIGO	IGCIAIGCCI	CAIC
mmommon	410	420	430	440	450
TICTIGI	TGGTTCTTCT	GGACTATCRA	AGGTATGTTG	CCCGTTTGTC	STCT
	460	470	480	490	500
AATTCC	AGGATCCTCAF	ACCACCAGCAG	CGGGACCATG	CCGAACCTGC	ATGA
	510	520	530		550
CTACTGC	TCAAGGAACC	TCTATGTAT	CCTCCTGTT	GCTGTACCAA	ACCT
	560	570	580		600
ACGGACG	GAAATTGCAC	CTGTATTCC	CATCCCATCA!	rcctgggctt:	rcgg
	610	620	630	640	650
AAAATTC	CTATGGGAGT	GGGCCTCAG	CCCGTTTCTC	CTGGCTCAGT:	TTAC
	660	670	680	690	700
TAGTGCC	CATTTGTTCAG	STGGTTCGTAC	EGGCTTTCCC(	CCACTGTTTG	SCTT
	710	720	730	740	750
TCAGTTA	ATATGGATGAT	GTGGTATTG(	GGGCCAAGT	CTGYACAGCA:	PCTT
	760	770	780	790	800
GAGTCCC	TTTTTACCGC	GGTGACCAA	TTTTCTTTTG	rctttgggta:	raca
	810	820	830	840	850
DAAATTT	CCTAACAAA	CAAAGAGAT	GGGTTACTC	rctgaatttt/	ATGG
	860	870	880	890	900
GTTATGI	CATTGGAAGI	TATGGGTCC	TTGCCACAAG	AACACATCAT	ACAA
	010				

910 AAAATCAAAGAA

#### 55 of 55

LSPNSARSPCWWLQFRNSKPCSDYCLSLIVNLLEDWGPCAEHGEHHIRIP RTPSRVTGGVFLVDKNPHNTAESRLVVDFSQFSRGNYRVSWPKFAVPNLQ SLTNLLSSNLSWLSLDVSAAFYHLPLHPAAMPHLLVGSSGLSRYVARLSS NSRILNHQHGTMPNLHDYCSRNLYVSLLLLYQTYGRKLHLYSHPIILGFR KIPMGVGLSPFLLAQFTSAICSVVRRAFPHCLAFSYMDDVVLGAKSXQHL ESLFTAVTNFLLSLGIHLNPNKTKRWGYSLNFMGYVIGSYGSLPQEHIIQ KIKE

### Figure 44

FHQTLQDPPAGG\$SSGTVNPVPTTASPLSSIFSRIGDPARNMENITSGFL GPLLVLQAGFFLLTRILTIPQSLDSWWTSLNFLGGTTVCLGQNSQSPTSN HSPTSCPPTCPGYRWMCLRRFIIFLFILLLCLIFLLVLLDYXGMLPVCPL IPGSSTTSTGPCRTCMTTAQGTSMYPSCCCTKPTDGNCTCIPIPSSWAFG KFLWEWASARFSWLSLLVPFVQWFVGLSPTVWLSVIWMMWYWGPSLXSIL SPFLPR*PIFFCLWVYI*

Figure 45